

FIG 5

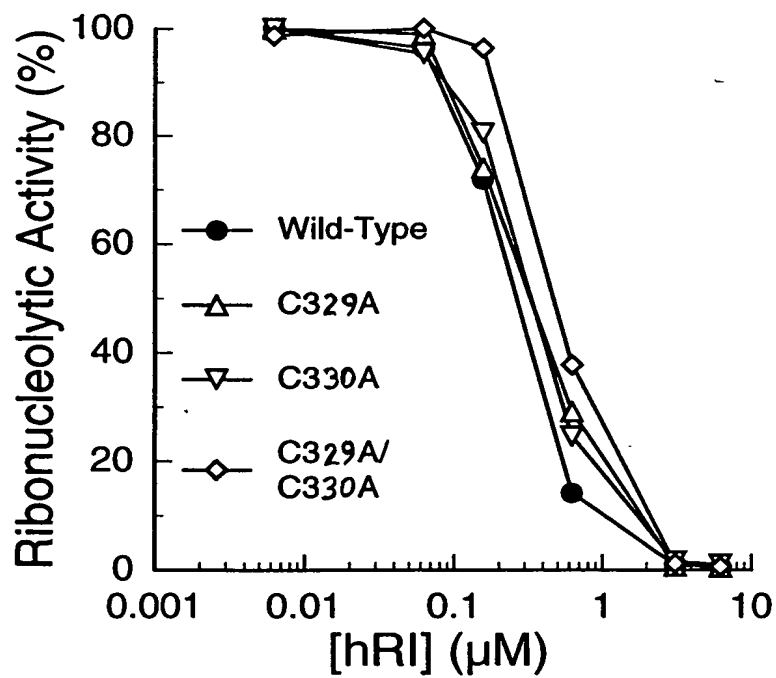
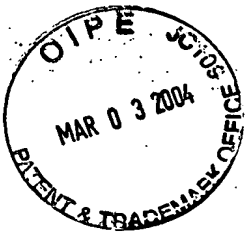


FIG 6



MSLDIQCEQLSDARWT---ELLPLIQQYQVVRLLDDCGLTEVRCKDIR
MNLDIHCQLSDARWT---ELLPLLQQYEVVRLLDDCGLTEEHCKDIG
MSLDIQSLOIQCEELSDARWA---ELLPLLQQCQVVRLLDDCGLTEARCKDIS

45 SATQANPAITELSLRTNELGDAGVGLVLQGLQNPCTCKIQKLSLQNCSLTEAGCGVLP
45 SALRANPSITELCLRTNELGDAGVHLVLQGLQSPTCKIQKLSLQNCSLTEAGCGVLP
50 SALRVNPALAEINLRSNELGDVGVMHCVLQGLQTPSCKIQKLSLQNCCLTGAGCGVLS

102 DVLRSLSLTIRELHLDNDNPLGDEGLKLLCEGLRDPQCRLEKLOLEYONLTATSCEPLA
102 SILRSLPTIRELHLSNDNPLGDAGLRLLCEGLLDPOCHLEKLOLEYORLTAASCEPLA
107 SILRTLPTLOELHLSNDNLLGDAGLQLLCEGLLDPOCRLEKLOLEYCSLSAASCEPLA

159 SVLRVKPDFKELVLSNNDFFHEAGIHTLCQGLKDSACQLESILKLENOGITSANCKDLC
159 SVLRATRAIKELIVSNNDIGEAGARVLGQGLADSACQLETIRLENOGLTPANCKDLC
164 SVLRAPDFKELIVSNNDINEAGVRVLQGLKDSPCQLEALKLES CGVTSDNCRDLC

216 DVVASKASLQELDLGSNKLGNLTGIAALCSGLLLPSCLRLRTLWLWDCDVTAEGCKDLC
216 GIVASQASLRELDLGSNGLGDAGIAELCPGLLSPASRLKTLWLWBCDITASGORDLC
221 GIVASKASLRELAIGSNKLGDVGMAELCPGLLHPSSRLRTLWIWECGITAKGCGDLC

273 RVLRAKQSLKELSLAGNELKDEGAQLLOESLLEPGCQLESILWVKTCSLTAASCPHFC
273 RVLQAKETLKELSLAGNKLGDGARLLCESLLQPGCQLESILWVKSCSLTAACQHVMS
278 RVLRAKESLKELSLAGNELGDGARLLCETLLEPGCQLESILWVKSCSFTAAACSHFS

330 SVLTKNSSLFELQSSNPLGDSGVVELOKALGYPDTVLRVLWLGD CDVTDSGCSSLA
330 LMLTQNKHLLELQSSNKLGDSGIQELQALSQPGTTLRVLQGDCEVTNSGCSSLA
335 SVLAQNRFLLELQISNNRLEDAGVRELQGLGQPGSVLRVLWLADCDVSDSSCSSLA

387 TVLLANRSLRELDLSNNCMGDNGVLQLLESILKQPSCLLQQLVLYDIYWTDEVEDQLR
387 SILLANRSLRELDLSNNCVGDPGVLLQGLSLEQPGCALEQLVLYDTYWTEEVEDRLQ
394 ATLLANHSLRELDLSNNCLGDAGILQLVESVRQPGCLLEQLVLYDIYWSEEMEDRLQ

444 ALEERPSLRITS 456 SEQ:10 NO:1
444 ALEGSKPGLRVIS 456 SEQ:10 NO:2
449 ALEKDKPSLRVIS 461 SEQ:10 NO:3

FIG 7